

SEQUENCE LISTING

<110> Chang, Chawnshang

<120> Androgen Receptor Coregulators

<130> 21108.0011U6

<140> 10/517,155

<141> 2005-01-06

<150> PCT/US03/17937

<151> 2003-06-06

<150> US 60/387,087

<151> 2002-06-06

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<223> Coding sequence and polypeptide region for the
C-terminal domain

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<223> Coding sequence and polypeptide region which may
form a cystein-rich RING finger motif

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<222> (964)...(1089)

<223> Coding sequence and polypeptide region for a
cystein-rich B box like structure

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Arg	Glu	Ala	Gln	Glu	Asp	Glu	Leu	Leu	Ala	Leu	Ala	Ser	Ile	Tyr	Asp	
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tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe 55 60 65	246
ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser 70 75 80 85	294
tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr 90 95 100	342
cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His 105 110 115	390
cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu 120 125 130	438
acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly 135 140 145	486
tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr 150 155 160 165	534
gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu 170 175 180	582
att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu 185 190 195	630
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ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys 295 300 305	966
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ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu 375 380 385	1206
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gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg Asp Glu Val Glu Asp *	1494
ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt tgccgggatat ttaggggtact attcattcac tcttctgctg tagaagatat ggaagaacga ggtttatatt ttcatgtggt actactgaag aaggtgcatt gatacathtt taaatgtaag ttgagaaaaa ttataagcc aaaggttcag aaaattaaac tacagaa	1554 1614 1674 1721

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65					70					75				80	
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Val	Ala	Thr	Pro	Gly	Gln	Val	Lys	Glu	Leu	Val	Glu	Ala	Glu	Leu	Phe
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Glu	Pro	Gly	Cys	Thr	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe
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Gln	Lys	Ala	Leu	Glu	Glu	Met	Glu	Ser	Lys	Glu	Trp	Leu	Glu	Lys	Asn
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Ser	Lys	Ser	Cys	Pro	Cys	Cys	Gly	Thr	Pro	Ile	Glu	Lys	Leu	Asp	Gly
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Cys	Asn	Lys	Met	Thr	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile
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 Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
 20 25 30
 tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag 144
 Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
 35 40 45

cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser 50 55 60	192
tcc agc ggt gtc ttg ggt acc ggg ctc tgt gag cta gat cgg ttg ctt Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu 65 70 75 80	240
cag gaa ctt aat gcc act cag ttc aac atc aca gat gaa atc atg tct Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser 85 90 95	288
cag ttc cca tct agc aag gtg gct tca gga gag cag aag gag gac cag Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln 100 105 110	336
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ctc cca aag gct tct gcc acc tca gcc act ctg gag ctg gat aga ctg Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu 130 135 140	432
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Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Phe Ser Ser 50 55 60
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu 65 70 75 80
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser 85 90 95

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Leu	Pro	Lys	Ala	Ser	Ala	Thr	Ser	Ala	Thr	Leu	Glu	Leu	Asp	Arg	Leu	130	135	140
Met	Ala	Ser	Leu	Pro	Asp	Phe	Arg	Val	Gln	Asn	His	Leu	Pro	Ala	Ser	145	150	155
Gly	Pro	Thr	Gln	Pro	Pro	Val	Val	Ser	Ser	Thr	Asn	Glu	Gly	Ser	Pro	165	170	175
Ser	Pro	Pro	Glu	Pro	Thr	Ala	Lys	Gly	Ser	Leu	Asp	Thr	Met	Leu	Gly	180	185	190
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Gly	Leu	Cys	Gly	Ser	Cys	Asn	Lys	Pro	Ile	Ala	Gly	Gln	Val	Val	Thr	210	215	220
Ala	Leu	Gly	Arg	Ala	Trp	His	Pro	Glu	His	Phe	Val	Cys	Gly	Gly	Cys	225	230	235
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Phe	Cys	Pro	Glu	Cys	Tyr	Phe	Glu	Arg	Phe	Ser	Pro	Arg	Cys	Gly	Phe	260	265	270
Cys	Asn	Gln	Pro	Ile	Arg	His	Lys	Met	Val	Thr	Ala	Leu	Gly	Thr	His	275	280	285
Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro	Phe	Gly	290	295	300
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Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Ala	Cys	Thr	Phe	405	410	415
Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala	Gly	Lys	420	425	430
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Gln Phe Lys Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr	
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Phe Val Lys Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala	
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acc ttg ggt gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga	195
Thr Leu Gly Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly	
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Arg Asp Leu Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly	
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Asn Lys Val Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val	
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Phe His Arg Lys Lys Asn Leu Gln Tyr Tyr Asp Ile Ser Ala Lys Ser	
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Asn Tyr Asn Phe Glu Lys Pro Phe Leu Trp Leu Ala Arg Lys Leu Ile	
155 160 165	
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Gly Asp Pro Asn Leu Glu Phe Val Ala Met Pro Ala Leu Ala Pro Pro	
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Glu Val Val Met Asp Pro Ala Leu Ala Ala Gln Tyr Glu His Asp Leu	
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Glu Val Ala Gln Thr Thr Ala Leu Pro Asp Glu Asp Asp Asp Leu	
205 210 215	
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Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
  35          40          45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
  50          55          60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
  65          70          75          80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
  85          90          95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
 100         105         110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
 115         120         125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
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Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
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Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
 165         170         175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
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Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
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acc gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc	218
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
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cct cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct	266
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro	
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Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala	
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Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp	
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Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr	
80 85 90	
att caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca gca	458
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala	
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gtt gac cta gat gag atg tcg ttc act ttt act gag cta cag aaa aac	506
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn	
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Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	
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Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	
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Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser	
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<211> 928

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Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65      70      75      80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85      90      95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
100     105     110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
115     120     125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
130     135     140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145     150     155     160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
165     170     175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
180     185     190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
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Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
				885					890					895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
			915				920						925		

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: note =
Oligonucleotide

<400> 9

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30

<210> 10

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: note =
synthetic construct

<400> 10

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27

<210> 11

<211> 32

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> 2-3, 6-13, 15, 17-18, 20-21, 23-28, 30-31

<223> Xaa can be any amino acid

<400> 11

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	His
1				5					10						15	
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Cys	
			20					25						30		

<210> 12

<211> 50

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> 2-3, 5-20, 22-23, 25-26, 28-29, 31-46, 48-49

<223> Xaa can be any amino acid

<400> 12

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15		
Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	
			35				40						45			
Xaa	Cys															
	50															

<210> 13

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13

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tcctccaacc	tccaagagtc	tgttttggga	ttgggttcag	gaatgaaatt	ctgcctgtgc	180
taacctcctg	gggagccggt	agacttgctt	gttaaaaatc	gcttctgctt	ttggagccta	240
aagcccggtt	ccgaaaaaca	agtggatatt	aggggaaaga	ggggtcttca	aaggctacag	300
tgagtcattc	cagccttcaa	ccatactacg	ccagcactac	gttctctaaa	gccactctgc	360
gctagcttgc	ggtgagggga	ggggagaaaa	ggaaagggga	ggggagggga	ggggagggag	420
aaaggaggtg	ggaaggcaga	gaggccggct	gcggggggcg	gaccgactca	caaactgttc	480
gatttcgttt	ccacctccca	gcgccccctc	ggagatccct	aggagccagc	ctgctgggag	540
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ctagccactc	cagtgccata	cagaagctta	agggacgcac	cacgccagcc	ccagcccagc	660
gacagccaac	gcctgttgca	gagcggcggc	ttcgaagccg	ccgcccagga	gctgcccttt	720
cctcttcggt	gaagtttcta	aaagctgcgg	gagactcaga	ggaagcaagg	aaagtgtccg	780
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ctaaaagaaa	acaaaaagaa	aatagcccag	ttcttatttg	cacctgcttc	agtggaacttt	1200
gaatttgga	ggcagaggat	ttcccctttt	ccctcccgtc	aaggtttgag	catcttttaa	1260

tctgttcttc	aagtatttag	agacaaactg	tgtaagtagc	agggcagatc	ctgtcttgcg	1320
cgtgccttcc	tttactggag	actttgaggt	tatctgggca	ctccccccac	ccaccccccc	1380
tctgtcaagt	tttcttcccc	ggagcttccc	gcaggtgggc	agctagctgc	agatactaca	1440
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<210> 14
 <211> 600
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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tcaggagact	
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cttgtcctgg	
tgggcccctgg	120
ggggagcggg	
gaggggaatac	
ctaagagcaa	
ttggtagctg	
gtacttctaa	
tgcctcttcc	180
tcttccaacc	
tccaagagtc	
tgttttgagg	
ttgggttcag	
gaatgaaatt	
ctgcctgtgc	240
taacctcctg	
gggagccggg	
agacttgtct	
gttaaaaatc	
gcttctgctt	
ttggagccta	300
aagcccgggt	
ccgaaaaaca	
agtggatatt	
aggggaaaga	
ggggctctca	
aaggctacag	360
tgatcattc	
cagccttcaa	
ccatactacg	
ccagcactac	
gttctctaaa	
gccactctgc	420
gctagcttgc	
ggtgagggga	
ggggagaaaa	
ggaaagggga	
ggggagggga	
ggggagggag	480
aaaggaggtg	
ggaaggcaga	
gaggccggct	
gcgggggcgg	
gaccgactca	
caaactgttc	540
gatttcgttt	
ccacctccca	
gcgccccctc	
ggagatccct	
aggagccagc	
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acctggaggc	
tgagagggca	
tcagagggga	
aaagactgag	

<210> 15
 <211> 359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

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taatcttgga	
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caattaaaaa	
tggcagaaac	
ttgtttgttg	
gaatacatgt	
gtgactcttg	
gtttgtctct	180
gcgtctggct	
ttagaaatgt	
catccattgt	
gtaaaatact	
ggcttggttg	
tctgccagct	240
aaaacttgcc	
acagcccctg	
ttgtgactgc	
aggctcaagt	
tattgttaac	
aaagagcccc	300
aagaaaagct	
gctaattgtc	
tcttatcacc	
attgttaatt	
tgtaaaaaca	
taaaacaatc	359
taaaatttca	
gatgaatgtc	
atcagagtgc	
ttttcattag	
ctctttttat	
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<210> 16
 <211> 899
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 16	
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20 25 30	
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala	
35 40 45	
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg	
50 55 60	

Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile	65	70	75	80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Gln	Pro	Ser	85	90	95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro	100	105	110	
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro	115	120	125	
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser		130	135	140	
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile	145	150	155	160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	165	170	175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln	180	185	190	
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr	195	200	205	
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr	210	215	220	
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	225	230	235	240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	245	250	255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val	260	265	270	
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu	275	280	285	
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser	290	295	300	
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	305	310	315	320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	325	330	335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	340	345	350	
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	355	360	365	
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	370	375	380	
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	385	390	395	400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	405	410	415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	420	425	430	
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser	435	440	445	
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	450	455	460	
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu	465	470	475	480
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	485	490	495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	500	505	510	
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	515	520	525	
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	530	535	540	

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gttatataac	tctgcactac	ttctctgcag	tgccttgggg	gaaattcctc	tactgatgta	2940
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<210> 18

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 18

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Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
			20					25					30		

Ala	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Asn	Ile	Ala
	35						40				45				
Pro	Pro	Gly	Ala	Cys	Leu	Gln	Gln	Arg	Gln	Glu	Thr	Ser	Pro	Arg	Arg
	50					55				60					
Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile
65					70					75					80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Gln	Pro	Ser
				85					90					95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro
			100					105					110		
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro
		115					120					125			
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser
	130					135					140				
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile
145					150					155					160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln
				165					170					175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln
			180					185					190		
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr
		195					200					205			
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr
	210					215					220				
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met
225					230					235					240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu
				245					250					255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Gly	Gly	Pro	Pro	Ala	Val	
			260				265						270		
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu
		275					280					285			
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser
	290					295					300				
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys
305					310					315					320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
				325					330					335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
			340				345						350		
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
		355					360					365			
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
	370					375					380				
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Gln	Cys	Arg	
385					390					395				400	
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
				405					410					415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe
			420					425					430		
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser
			435					440				445			
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
	450					455					460				
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu
465					470					475					480
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro
				485					490					495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly
			500					505					510		

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Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
   515                               520                   525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
   530                               535                   540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545                               550                   555                   560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
   565                               570                   575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
   580                               585                   590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
   595                               600                   605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
   610                               615                   620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625                               630                   635                   640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
   645                               650                   655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
   660                               665                   670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
   675                               680                   685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
   690                               695                   700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705                               710                   715                   720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
   725                               730                   735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
   740                               745                   750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
   755                               760                   765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
   770                               775                   780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785                               790                   795                   800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
   805                               810                   815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
   820                               825                   830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
   835                               840                   845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
   850                               855                   860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865                               870                   875                   880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
   885                               890                   895
His Thr Gln

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<210> 19

<211> 2988

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

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aaagacattt	tgaacgagc	cggcaccatg	caacttcttc	agcagcagca	acaacagcag	660
cagcaccaac	agcagcacca	acagcaccaa	cagcagcagg	aggtaatctc	cgaaggcagc	720
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<210> 20

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

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Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	515	520	525
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	530	535	540
Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	545	550	555
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	565	570	575
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	580	585	590
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	595	600	605
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	610	615	620
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr	625	630	635
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	645	650	655
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	660	665	670
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	675	680	685
Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	690	695	700
Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	705	710	715
Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn	725	730	735
Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu	740	745	750
Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg	755	760	765
His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe	770	775	780
Leu	Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	785	790	795
Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys	805	810	815
Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys	820	825	830
Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro	835	840	845
Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser	850	855	860
His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser	865	870	875
Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe	885	890	895

His Thr Gln

<210> 21

<211> 2700

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

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<210> 22

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 22

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<210> 23

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 23

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Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
          20          25          30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
          35          40          45
Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln Glu Thr
          50          55          60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
          65          70          75          80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
          85          90          95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
          100          105          110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
          115          120          125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
          130          135          140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
          145          150          155          160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
          165          170          175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
          180          185          190
Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
          195          200          205
Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
          210          215          220
Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
          225          230          235          240
Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
          245          250          255
Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
          260          265          270
Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
          275          280          285
Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
          290          295          300

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Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu	Glu	Gly	305	310	315	320
Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	Gly	Thr	325	330	335	
Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	340	345	350	
Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	355	360	365	
Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His	Ala	Arg	370	375	380	
Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	385	390	395	400
Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Ala	Gly	405	410	415	
Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	Ser	Ser	420	425	430	
Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Cys	435	440	445	
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	450	455	460	
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	Tyr	465	470	475	480
Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	Phe	485	490	495	
Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro	500	505	510	
Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp	515	520	525	
Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp	530	535	540	
His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	545	550	555	560
Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	565	570	575	
Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	580	585	590	
Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	595	600	605	
Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	610	615	620	
Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	625	630	635	640
Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr	645	650	655	
Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	660	665	670	
Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	675	680	685	
His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	690	695	700	
Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	705	710	715	720
Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	725	730	735	
Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	740	745	750	
Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	755	760	765	
Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	770	775	780	

Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	785	790	795	800
Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu	Leu	Leu	Phe	Ser	Ile	Ile		805	810	815
Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	820	825	830	
Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	835	840	845	
Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	850	855	860	
Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	865	870	875	880
Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	885	890	895	
Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	900	905	910	
Pro	Ile	Tyr	Phe	His	Thr	Gln										915			

<210> 24

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 24

Met	Thr	Met	Thr	Leu	His	Thr	Lys	Ala	Ser	Gly	Met	Ala	Leu	Leu	His	1	5	10	15
Gln	Ile	Gln	Gly	Asn	Glu	Leu	Glu	Pro	Leu	Asn	Arg	Pro	Gln	Leu	Lys	20	25	30	
Ile	Pro	Leu	Glu	Arg	Pro	Leu	Gly	Glu	Val	Tyr	Leu	Asp	Ser	Ser	Lys	35	40	45	
Pro	Ala	Val	Tyr	Asn	Tyr	Pro	Glu	Gly	Ala	Ala	Tyr	Glu	Phe	Asn	Ala	50	55	60	
Ala	Ala	Ala	Ala	Asn	Ala	Gln	Val	Tyr	Gly	Gln	Thr	Gly	Leu	Pro	Tyr	65	70	75	80
Gly	Pro	Gly	Ser	Glu	Ala	Ala	Ala	Phe	Gly	Ser	Asn	Gly	Leu	Gly	Gly	85	90	95	
Phe	Pro	Pro	Leu	Asn	Ser	Val	Ser	Pro	Ser	Pro	Leu	Met	Leu	Leu	His	100	105	110	
Pro	Pro	Pro	Gln	Leu	Ser	Pro	Phe	Leu	Gln	Pro	His	Gly	Gln	Gln	Val	115	120	125	
Pro	Tyr	Tyr	Leu	Glu	Asn	Glu	Pro	Ser	Gly	Tyr	Thr	Val	Arg	Glu	Ala	130	135	140	
Gly	Pro	Pro	Ala	Phe	Tyr	Arg	Pro	Asn	Ser	Asp	Asn	Arg	Arg	Gln	Gly	145	150	155	160
Gly	Arg	Glu	Arg	Leu	Ala	Ser	Thr	Asn	Asp	Lys	Gly	Ser	Met	Ala	Met	165	170	175	
Glu	Ser	Ala	Lys	Glu	Thr	Arg	Tyr	Cys	Ala	Val	Cys	Asn	Asp	Tyr	Ala	180	185	190	
Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	195	200	205	
Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	Asp	Tyr	Met	Cys	Pro	Ala	Thr	210	215	220	
Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys	Gln	Ala	Cys	225	230	235	240
Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val	Gly	Met	Met	Lys	Gly	Gly	Ile	Arg	245	250	255	

Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
260 265 270
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
275 280 285
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
290 295 300
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
305 310 315 320
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
325 330 335
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
340 345 350
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
355 360 365
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
370 375 380
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
385 390 395 400
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
405 410 415
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
420 425 430
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
435 440 445
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
450 455 460
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
465 470 475 480
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
485 490 495
Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
500 505 510
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
515 520 525
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
530 535 540
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545 550 555 560
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
565 570 575
His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
580 585 590
Ala Thr Val
595

<210> 25

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 25

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gccggcttca	ccggaccgca	ggctcccggg	gcagggccgg	ggccagagct	cgcgtgtcgg	240
cgggacatgc	gctgcgtcgc	ctctaacctc	gggctgtgct	ctttttccag	gtggcccgc	300
ggttttctgag	ccttctgccc	tgcggggaca	cgggtctgcac	cctgcccgcg	gccacggacc	360

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taaggtgttc tcaccttgaa atcttataca ctgaaatggc cattgattta ggccactggc 5460
ttagagtact ccttcccctg catgacactg attacaaata ctttccctatt catactttcc 5520
aattatgaga tggactgtgg gtactgggag tgatcactaa caccatagta atgtctaata 5580
ttcacaggca gatctgcttg ggaagctag ttatgtgaaa ggcaataaaa gtcatacagt 5640
agctcaaaag gcaaccataa ttctcttttg tgcaagtctt gggagcgtga tctagattac 5700
actgcaccaa tcccaagtta atcccctgaa aacttactct caactggagc aaatgaactt 5760
tgggtcccaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc 5820
ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta 5880
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tctattcatt tttttgcac caattgtgcc tgaactttta aaatatgtaa atgctgccat 6000
gttccaaacc catcgtcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt 6060
gtcccatgag caggtgcctg agacacagac ccctttgcat tcacagagag gtcattgggt 6120
atagagactt gaattaataa gtgacattat gccagtttct gttctctcac aggtgataaa 6180
caatgctttt tgtgcactac atactcttca gtgtagagct cttgttttat gggaaaaggc 6240
tcaaagtcca aattgtgttt gatggattaa tatgcccttt tgcgatgca tactattact 6300
gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgcacttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac 6420
ctatttgatg ttcaaataaa gaattaaact 6450

```

<210> 26

<211> 614

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 26

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Met Asn Thr Phe Gln Asp Gln Ser Gly Ser Ser Ser Asn Arg Glu Pro
 1              5              10              15
Leu Leu Arg Cys Ser Asp Ala Arg Arg Asp Leu Glu Leu Ala Ile Gly
              20              25              30
Gly Val Leu Arg Ala Glu Gln Gln Ile Lys Asp Asn Leu Arg Glu Val
              35              40              45

```

Lys	Ala	Gln	Ile	His	Ser	Cys	Ile	Ser	Arg	His	Leu	Glu	Cys	Leu	Arg
50						55					60				
Ser	Arg	Glu	Val	Trp	Leu	Tyr	Glu	Gln	Val	Asp	Leu	Ile	Tyr	Gln	Leu
65					70					75					80
Lys	Glu	Glu	Thr	Leu	Gln	Gln	Gln	Ala	Gln	Gln	Leu	Tyr	Ser	Leu	Leu
				85					90					95	
Gly	Gln	Phe	Asn	Cys	Leu	Thr	His	Gln	Leu	Glu	Cys	Thr	Gln	Asn	Lys
			100					105					110		
Asp	Leu	Ala	Asn	Gln	Val	Ser	Val	Cys	Leu	Glu	Arg	Leu	Gly	Ser	Leu
	115						120					125			
Thr	Leu	Lys	Pro	Glu	Asp	Ser	Thr	Val	Leu	Leu	Phe	Glu	Ala	Asp	Thr
	130					135					140				
Ile	Thr	Leu	Arg	Gln	Thr	Ile	Thr	Thr	Phe	Gly	Ser	Leu	Lys	Thr	Ile
145					150					155					160
Gln	Ile	Pro	Glu	His	Leu	Met	Ala	His	Ala	Ser	Ser	Ala	Asn	Ile	Gly
				165					170					175	
Pro	Phe	Leu	Glu	Lys	Arg	Gly	Cys	Ile	Ser	Met	Pro	Glu	Gln	Lys	Ser
	180						185							190	
Ala	Ser	Gly	Ile	Val	Ala	Val	Pro	Phe	Ser	Glu	Trp	Leu	Leu	Gly	Ser
	195						200					205			
Lys	Pro	Ala	Ser	Gly	Tyr	Gln	Ala	Pro	Tyr	Ile	Pro	Ser	Thr	Asp	Pro
	210					215					220				
Gln	Asp	Trp	Leu	Thr	Gln	Lys	Gln	Thr	Leu	Glu	Asn	Ser	Gln	Thr	Ser
225					230					235					240
Ser	Arg	Ala	Cys	Asn	Phe	Phe	Asn	Asn	Val	Gly	Gly	Asn	Leu	Lys	Gly
			245						250					255	
Leu	Glu	Asn	Trp	Leu	Leu	Lys	Ser	Glu	Lys	Ser	Ser	Tyr	Gln	Lys	Cys
		260						265					270		
Asn	Ser	His	Ser	Thr	Thr	Ser	Ser	Phe	Ser	Ile	Glu	Met	Glu	Lys	Val
	275						280					285			
Gly	Asp	Gln	Glu	Leu	Pro	Asp	Gln	Asp	Glu	Met	Asp	Leu	Ser	Asp	Trp
	290					295					300				
Leu	Val	Thr	Pro	Gln	Glu	Ser	His	Lys	Leu	Arg	Lys	Pro	Glu	Asn	Gly
305					310					315					320
Ser	Arg	Glu	Thr	Ser	Glu	Lys	Phe	Lys	Leu	Leu	Phe	Gln	Ser	Tyr	Asn
			325						330					335	
Val	Asn	Asp	Trp	Leu	Val	Lys	Thr	Asp	Ser	Cys	Thr	Asn	Cys	Gln	Gly
	340							345					350		
Asn	Gln	Pro	Lys	Gly	Val	Glu	Ile	Glu	Asn	Leu	Gly	Asn	Leu	Lys	Cys
	355						360					365			
Leu	Asn	Asp	His	Leu	Glu	Ala	Lys	Lys	Pro	Leu	Ser	Thr	Pro	Ser	Met
	370					375						380			
Val	Thr	Glu	Asp	Trp	Leu	Val	Gln	Asn	His	Gln	Asp	Pro	Cys	Lys	Val
385					390					395					400
Glu	Glu	Val	Cys	Arg	Ala	Asn	Glu	Pro	Cys	Thr	Ser	Phe	Ala	Glu	Cys
			405						410					415	
Val	Cys	Asp	Glu	Asn	Cys	Glu	Lys	Glu	Ala	Leu	Tyr	Lys	Trp	Leu	Leu
		420						425					430		
Lys	Lys	Glu	Gly	Lys	Asp	Lys	Asn	Gly	Met	Pro	Val	Glu	Pro	Lys	Pro
	435						440					445			
Glu	Pro	Glu	Lys	His	Lys	Asp	Ser	Leu	Asn	Met	Trp	Leu	Cys	Pro	Arg
	450					455					460				
Lys	Glu	Val	Ile	Glu	Gln	Thr	Lys	Ala	Pro	Lys	Ala	Met	Thr	Pro	Ser
465					470					475					480
Arg	Ile	Ala	Asp	Ser	Phe	Gln	Val	Ile	Lys	Asn	Ser	Pro	Leu	Ser	Glu
			485						490					495	
Trp	Leu	Ile	Arg	Pro	Pro	Tyr	Lys	Glu	Gly	Ser	Pro	Lys	Glu	Val	Pro
			500					505					510		
Gly	Thr	Glu	Asp	Arg	Ala	Gly	Lys	Gln	Lys	Phe	Lys	Ser	Pro	Met	Asn
	515						520					525			

Thr	Ser	Trp	Cys	Ser	Phe	Asn	Thr	Ala	Asp	Trp	Val	Leu	Pro	Gly	Lys
530						535					540				
Lys	Met	Gly	Asn	Leu	Ser	Gln	Leu	Ser	Ser	Gly	Glu	Asp	Lys	Trp	Leu
545					550					555					560
Leu	Arg	Lys	Lys	Ala	Gln	Glu	Val	Leu	Leu	Asn	Ser	Pro	Leu	Gln	Glu
				565					570					575	
Glu	His	Asn	Phe	Pro	Pro	Asp	His	Tyr	Gly	Leu	Pro	Ala	Val	Cys	Asp
			580					585					590		
Leu	Phe	Ala	Cys	Met	Gln	Leu	Lys	Val	Asp	Lys	Glu	Lys	Trp	Leu	Tyr
	595					600						605			
Arg	Thr	Pro	Leu	Gln	Met										
610															

<210> 27
 <211> 1845
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 27																
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agtgatgcac	ggagggactt	ggagcttgct	attggtggag	ttctccgggc	tgaacagcaa											120
attaaagata	acttgcgaga	ggtcaaagct	cagattcaca	gttgcataag	ccgtcacctg											180
gaatgtctta	gaagccgtga	ggtatggctg	tatgaacagg	tggaccttat	ttatcagctt											240
aaagaggaga	cacttcaaca	gcaggctcag	cagctctact	cgttattggg	ccagttcaat											300
tgtcttactc	atcaactgga	gtgtacccaa	aacaaagatc	tagccaatca	agtctctgtg											360
tgcttgga	gactgggcag	tttgaccctt	aagcctgaag	attcaactgt	cctgctcttt											420
gaagctgaca	caattactct	gcgccagacc	atcaccacat	ttgggtctct	caaaaccatt											480
caaattcctg	agcacttgat	ggctcatgct	agttcagcaa	atattggggc	cttcctggag											540
aagagaggct	gtatctccat	gccagagcag	aagtcagcat	ccggtattgt	agctgtccct											600
ttcagcgaat	ggctccttgg	aagcaaacct	gccagtgggt	atcaagctcc	ttacataccc											660
agcaccgacc	cccaggactg	gcttacccaa	aagcagacct	tggagaacag	tcagacttct											720
tccagagcct	gcaatttctt	caataatgtc	gggggaaacc	taaagggtct	agaaaactgg											780
ctcctcaaga	gtgaaaaatc	aagttatcaa	aagtgttaaca	gccattccac	tactagttct											840
ttctccattg	aaatggaaaa	ggttgagat	caagagcttc	ctgatcaaga	tgagatggac											900
ctatcagatt	ggctagtgtg	tccccaggaa	tcccataagc	tgcggaagcc	tgagaatggc											960
agtcgtgaaa	ccagtgtgaa	gtttaagctc	ttattccagt	cctataatgt	gaatgattgg											1020
cttgtcaaga	ctgactcctg	taccaactgt	cagggaaacc	agcccaaagg	tgtggagatt											1080
gaaaaccttg	gcaatctgaa	gtgcctgaat	gaccacttgg	aggccaagaa	accattgtcc											1140
acccccagca	tggttacaga	ggattggctt	gtccagaacc	atcaggaccc	atgtaaggta											1200
gaggaggtgt	gcagagccaa	tgagccctgc	acaagctttg	cagagtgtgt	gtgtgatgag											1260
aattgtgaga	aggaggctct	gtataagtgg	cttctgaaga	aagaaggaaa	ggataaaaaat											1320
gggatgcctg	tggaaaccaa	acctgagcct	gagaagcata	aagattccct	gaatatgtgg											1380
ctctgtccta	gaaaagaagt	aatagaacaa	actaaagcac	caaaggcaat	gactccttct											1440
agaattgctg	attccttcca	agtcataaag	aacagccctt	tgctggagtgt	gcttatcagg											1500
ccccataaca	aagaaggaag	tcccaaggaa	gtgcctggta	ctgaagacag	agctggcaaa											1560
cagaagttaa	aaagcccat	gaatacttcc	tggtgttctt	ttaacacagc	tgactgggtc											1620
ctgccaggaa	agaagatggg	caacctcagc	cagttatctt	ctggagaaga	caagtggctg											1680
cttcgaaaga	aggcccagga	agtattactt	aattcacctc	tacaggagga	acataacttc											1740
ccccagacc	attatggcct	ccctgcagtt	tgtgatctct	ttgcctgtat	gcagcttaaa											1800
gttgataaag	agaagtgggt	atatcgaact	cctctacaga	tgtga												1845

<210> 28
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>

38

Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
 450 455 460
 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
 465 470

<210> 29
 <211> 1701
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 29
 ggtctctggt ctcccctctc tgagcactct gaggtcctta tgtcgtcaga agatcgagaa 60
 gctcaggagg atgaattgct ggccctggca agtattttacg atggagatga atttagaaaa 120
 gcagagtctg tccaagggtg agaaaccagg atctattttg atttgccaca gaatttcaag 180
 atatttgtga gcggcaattc aaatgagtggt ctccagaata gtggctttga atacaccatt 240
 tgctttctgc ctccacttgt gctgaacttt gaactgccac cagattatcc atcctcttcc 300
 ccaccttcat tcacacttag tggcaaattg ctgtcaccaa ctcagctatc tgctctatgc 360
 aagcacttag acaacctatg ggaagaacac cgtggcagcg tggctcctgtt tgcctggatg 420
 caattttctta aggaagagac cctagcatac ttgaatattg tctctccttt tgagctcaag 480
 attggttctc agaaaaaagt gcagagaagg acagctcaag cttctcccaa cacagagcta 540
 gattttggag gagctgctgg atctgatgta gaccaagagg aaattgtgga tgagagagca 600
 gtgcaggatg tggaatcact gtcaaactct atccaggaaa tcttggactt tgatcaagct 660

 cagcagataa aatgctttta tagtaaattg ttcctgtgca gtatctgttt ctgtgagaag 720
 ctgggtagtg aatgcatgta cttcttggag tgcaggcatg tgtactgcaa agcctgtctg 780
 aaggactact ttgaaatcca gatcagagat ggccagggtc aatgcctcaa ctgccagaa 840
 ccaaagtgcc cttcgggtggc cactcctggt cagggtcaaag agttagtga agcagagtta 900
 tttgcccgtt atgaccgcct tctcctccag tctccttgg acctgatggc agatgtggtg 960
 tactgcccc ggccgtgctg ccagctgcct gtgatgcagg aacctggctg caccatgggt 1020
 atctgctcca gctgcaattt tgccctctgt actttgtgca gggttgaccta ccatgggggtc 1080
 tccccatgta aggtgactgc agagaaatta atggacttac gaaatgaata cctgcaagcg 1140
 gatgaggcta ataaaagact tttggatcaa aggtatggta agagagtga tcagaaggca 1200
 ctggaagaga tggaaagtaa ggagtggcta gagaagaact caaagagctg cccatgttgt 1260
 ggaactccca tagagaaatt agacggatgt aacaagatga catgtactgg ctgtatgcaa 1320
 tatttctggt ggatttgcatt gggttctctc tctagagcaa acccttacia acatttcaat 1380
 gacctggtt caccatgttt taaccggctg ttttatgctg tggatgttga cgacgatatt 1440
 tgggaagatg aggtagaaga ctagttaact actgctcaag atatggaagt ggattgtttt 1500
 tcctaatct tccgtcaagt acacaaagta actttgcggg atatttaggg tactattcat 1560
 tcaactctcc tgcgtagaag atatggaaga acgaggttta tattttcatg tggtagtact 1620
 gaagaagggt cattgatata tttttaaatg taagttgaga aaaatttata agccaaaggt 1680
 tcagaaaatt aaactacaga a 1701

<210> 30
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 30
 Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
 1 5 10 15
 Pro Pro Pro Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser
 20 25 30

Ser	Gly	Ala	Ser	Gly	Asp	Lys	Asp	His	Leu	Tyr	Ser	Thr	Val	Cys	Lys
	35						40					45			
Pro	Arg	Ser	Pro	Lys	Pro	Ala	Ala	Pro	Ala	Ala	Pro	Pro	Phe	Ser	Ser
	50					55					60				
Ser	Ser	Gly	Val	Leu	Gly	Thr	Gly	Leu	Cys	Glu	Leu	Asp	Arg	Leu	Leu
65					70					75					80
Gln	Glu	Leu	Asn	Ala	Thr	Gln	Phe	Asn	Ile	Thr	Asp	Glu	Ile	Met	Ser
			85						90					95	
Gln	Phe	Pro	Ser	Ser	Lys	Val	Ala	Ser	Gly	Glu	Gln	Lys	Glu	Asp	Gln
		100						105					110		
Ser	Glu	Asp	Lys	Lys	Arg	Pro	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Pro	Gly
		115					120					125			
Leu	Pro	Lys	Ala	Ser	Ala	Thr	Ser	Ala	Thr	Leu	Glu	Leu	Asp	Arg	Leu
	130					135					140				
Met	Ala	Ser	Leu	Pro	Asp	Phe	Arg	Val	Gln	Asn	His	Leu	Pro	Ala	Ser
145					150					155					160
Gly	Pro	Thr	Gln	Pro	Pro	Val	Val	Ser	Ser	Thr	Asn	Glu	Gly	Ser	Pro
			165					170						175	
Ser	Pro	Pro	Glu	Pro	Thr	Ala	Lys	Gly	Ser	Leu	Asp	Thr	Met	Leu	Gly
		180					185						190		
Leu	Leu	Gln	Ser	Asp	Leu	Ser	Arg	Arg	Gly	Val	Pro	Thr	Gln	Ala	Lys
	195						200					205			
Gly	Leu	Cys	Gly	Ser	Cys	Asn	Lys	Pro	Ile	Ala	Gly	Gln	Val	Val	Thr
	210					215					220				
Ala	Leu	Gly	Arg	Ala	Trp	His	Pro	Glu	His	Phe	Val	Cys	Gly	Gly	Cys
225					230					235					240
Ser	Thr	Ala	Leu	Gly	Gly	Ser	Ser	Phe	Phe	Glu	Lys	Asp	Gly	Ala	Pro
			245					250						255	
Phe	Cys	Pro	Glu	Cys	Tyr	Phe	Glu	Arg	Phe	Ser	Pro	Arg	Cys	Gly	Phe
		260					265						270		
Cys	Asn	Gln	Pro	Ile	Arg	His	Lys	Met	Val	Thr	Ala	Leu	Gly	Thr	His
	275						280					285			
Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro	Phe	Gly
	290					295					300				
Asp	Glu	Gly	Phe	His	Glu	Arg	Glu	Gly	Arg	Pro	Tyr	Cys	Arg	Arg	Asp
305					310					315					320
Phe	Leu	Gln	Leu	Phe	Ala	Pro	Arg	Cys	Gln	Gly	Cys	Gln	Gly	Pro	Ile
			325					330						335	
Leu	Asp	Asn	Tyr	Ile	Ser	Ala	Leu	Ser	Leu	Leu	Trp	His	Pro	Asp	Cys
		340					345						350		
Phe	Val	Cys	Arg	Glu	Cys	Phe	Ala	Pro	Phe	Ser	Gly	Gly	Ser	Phe	Phe
		355					360					365			
Glu	His	Glu	Gly	Arg	Pro	Leu	Cys	Glu	Asn	His	Phe	His	Ala	Arg	Arg
	370					375					380				
Gly	Ser	Leu	Trp	Pro	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg	Cys	Val
385					390					395					400
Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Ala	Cys	Thr	Phe
			405					410						415	
Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala	Gly	Lys
		420					425						430		
Pro	Tyr	Cys	Gln	Pro	Cys	Phe	Leu	Lys	Leu	Phe	Gly				
	435						440								

<210> 31

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 31

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atgccaaaggt cagggggctcc caaagagcgc cctgcggagc ctctcacccc tcccccatcc      60

tatggccacc agccacagac aggggtctggg gagtcttcag gagcctcggg ggacaaggac      120
cacctgtaca gcacggtatg caagcctcgg tccccaaagc ctgcagcccc ggccgcccct      180
ccattctcct cttccagcgg tgtcttgggt accgggctct gtgagctaga tcggttgctt      240
caggaactta atgccactca gttcaacatc acagatgaaa tcatgtctca gttcccatct      300
agcaaggtgg cttcaggaga gcagaaggag gaccagtctg aagataagaa aagaccagc      360
ctcccttcca gcccgtctcc tggcctccca aaggcttctg ccacctcagc cactctggag      420
ctggatagac tgatggcctc actccctgac ttccgcgttc aaaaccatct tccagcctct      480
gggccaaactc agccaccggt ggtgagctcc acaaatgagg gctcccccac cccaccagag      540
ccgactgcaa agggcgagcct agacaccatg ctggggctgc tgcagtccga cctcagccgc      600
cggggtgttc ccaccaggc caaaggcctc tgtggctcct gcaataaacc tattgtctggg      660
caagtggatga cggctctggg ccgcgcctgg caccctcagc acttcgtttg cggaggctgt      720
tccaccgccc tgggaggcag cagcttcttc gagaaggatg gagccccctt ctgccccgag      780
tgctactttg agcgcttctc gccaaagatgt ggcttctgca accagcccat ccgacacaag      840
atggtgaccg ccttgggcac tctactggcag ccagagcatt tctgctgcgt cagttgcggg      900
gagcccttcg gagatgaggg tttccacgag cgcgagggcc gccctactg ccgcggggac      960
ttcttgacgc tgttcgcccc gcgtgcccag ggctgcccag gcccctactg ggataactac     1020
atctcgcgcc tcagcctgct ctggcaccgg gactgtttcg tctgcaggga atgcttcgcg     1080
cccttctcgg gaggcagcct tttcagacac gagggcgccc cgttgtgcga gaaccacttc     1140
cacgcacgac gcggctcgtc gtggcccacg tgtggcctcc ctgtgaccgg ccgctgcgtg     1200
tcggccctgg gtcgcccgtt ccaccgggac cacttcgcat gcaccttctg cctgcgcccg     1260
ctcaccaagg ggtccttcca ggagcgcgcc ggcaagccct actgccagcc ctgcttctcg     1320
aagctcttcg gctga                                     1335

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<210> 32

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 32

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Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
 1              5              10              15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
      20              25              30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
      35              40              45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
      50              55              60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
      65              70              75              80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
      85              90              95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
      100             105             110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
      115             120             125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
      130             135             140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
      145             150             155             160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
      165             170             175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
      180             185             190

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Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
 195 200 205
 Leu Pro Asp Glu Asp Asp Asp Leu
 210 215

<210> 33
 <211> 1566
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 33
 ggcgcttctg gaaggaacgc cgcgatggct ggcgagggag agccccaggt ccagttcaaa 60
 cttgtatttg ttggtgatgg tggtagcaga aaaacgacct tcgtgaaacg tcatttgact 120
 ggtgaatttg agaagaagta ttagaccacc ttgggtggtg aggttcatcc cctagtgttc 180
 cacaccaaca gaggacctat taagttcaat gtatgggaca cagccggcca ggagaaattc 240
 ggtggactga gagatggcta ttatatccaa gccagtggtg ccatcataat gtttgatgta 300
 acatcgagag ttactttaca gaatgtgcct aactggcata gagatctggt acgagtgtgt 360
 gaaaacatcc ccattgtggt gtgtggcaac aaagtggata ttaaggacag gaaagtgaag 420
 gcgaaatcca ttgtcttcca ccgaaagaag aatcttcagt actacgacat ttctgcaaaa 480
 agtaactaca actttgaaaa gcccttcctc tggcttgcta ggaagctcat tggagaccct 540
 aacttggaat ttgttgccat gcctgctctc gcccaccag aagttgtcat ggaccagct 600
 ttggcagcac agtatgagca cgacttagag gttgctcaga caactgctct cccggatgag 660
 gatgatgacc tgtgagaatg aagctggagc ccagcgtcag aagtctagtt ttataggcag 720
 ctgtcctgtg atgtcagcgg tgcagcgtgt gtgccacctc attattatct agctaagcgg 780
 aacatgtgct ttatctgtgg gatgctgaag gagatgagtg ggcttcggag tgaatgtggc 840
 agtttaaaaa ataacttcat tgtttggacc tgcataattta gctgtttgga cgcagttgat 900
 tccttgagtt tcatatataa gactgctgca gtcacatcac aatattcagt ggtgaaatct 960
 tgtttgttac tgtcattccc attccttttc tttagaatca gaataaagtt gtatttcaaa 1020
 tatctaagca agtgaactca tcccttggtt ataaatagca tttggaaacc actaaagtag 1080
 ggaagtttta tgccatgtta atatttgaat tgccttgctt ttatcactta atttgaaatc 1140
 tattgggtta atttctccct atgtttatth ttgtacattt gagccatgtc acacaaactg 1200
 atgatgacag gtcagcagta ttctatttgg ttagaagggt tacatgggtg aaatatagtt 1260
 gcagttaagc taaagcagtg tttgctccac ctccatattg gctaggtagg gtcacctagg 1320
 gaagcacttg ctcaaaaatct gtgacctgac agaataaaaa tgtggtttgt acatatcaaa 1380
 tagatatattt aagggttaata ttttctttta tggcaaaagt aatcatgttt taatgtagaa 1440
 cctcaaacag gatggaacat cagtggatgg caggaggttg ggaattcttg ctgttaaaaa 1500
 taattacaaa ttttgcaactt tttgtttgaa tgtttagatgc ttagtgtgaa gttgatacgc 1560
 aagccg 1566

<210> 34
 <211> 2427
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 34
 Met Pro Leu Lys Thr Arg Thr Ala Leu Ser Asp Asp Pro Asp Ser Ser
 1 5 10 15
 Thr Ser Thr Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser
 20 25 30
 Ser Thr Ser Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr
 35 40 45
 Pro Leu Lys Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg
 50 55 60

Arg	Pro	Trp	Trp	Pro	Cys	Arg	Ile	Cys	Ser	Asp	Pro	Leu	Ile	Asn	Thr	65	70	75	80
His	Ser	Lys	Met	Lys	Val	Ser	Asn	Arg	Arg	Pro	Tyr	Arg	Gln	Tyr	Tyr	85	90	95	
Val	Glu	Ala	Phe	Gly	Asp	Pro	Ser	Glu	Arg	Ala	Trp	Val	Ala	Gly	Lys	100	105	110	
Ala	Ile	Val	Met	Phe	Glu	Gly	Arg	His	Gln	Phe	Glu	Glu	Leu	Pro	Val	115	120	125	
Leu	Arg	Arg	Arg	Gly	Lys	Gln	Lys	Glu	Lys	Gly	Tyr	Arg	His	Lys	Val	130	135	140	
Pro	Gln	Lys	Ile	Leu	Ser	Lys	Trp	Glu	Ala	Ser	Val	Gly	Leu	Ala	Glu	145	150	155	160
Gln	Tyr	Asp	Val	Pro	Lys	Gly	Ser	Lys	Asn	Arg	Lys	Cys	Ile	Pro	Gly	165	170		175
Ser	Ile	Lys	Leu	Asp	Ser	Glu	Glu	Asp	Met	Pro	Phe	Glu	Asp	Cys	Thr	180	185		190
Asn	Asp	Pro	Glu	Ser	Glu	His	Asp	Leu	Leu	Leu	Asn	Gly	Cys	Leu	Lys	195	200	205	
Ser	Leu	Ala	Phe	Asp	Ser	Glu	His	Ser	Ala	Asp	Glu	Lys	Glu	Lys	Pro	210	215	220	
Cys	Ala	Lys	Ser	Arg	Ala	Arg	Lys	Ser	Ser	Asp	Asn	Pro	Lys	Arg	Thr	225	230	235	240
Ser	Val	Lys	Lys	Gly	His	Ile	Gln	Phe	Glu	Ala	His	Lys	Asp	Glu	Arg	245	250		255
Arg	Gly	Lys	Ile	Pro	Glu	Asn	Leu	Gly	Leu	Asn	Phe	Ile	Ser	Gly	Asp	260	265	270	
Ile	Ser	Asp	Thr	Gln	Ala	Ser	Asn	Glu	Leu	Ser	Arg	Ile	Ala	Asn	Ser	275	280	285	
Leu	Thr	Gly	Ser	Asn	Thr	Ala	Pro	Gly	Ser	Phe	Leu	Phe	Ser	Ser	Cys	290	295	300	
Gly	Lys	Asn	Thr	Ala	Lys	Lys	Glu	Phe	Glu	Thr	Ser	Asn	Gly	Asp	Ser	305	310	315	320
Leu	Leu	Gly	Leu	Pro	Glu	Gly	Ala	Leu	Ile	Ser	Lys	Cys	Ser	Arg	Glu	325	330	335	
Lys	Asn	Lys	Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu	340	345	350	
Cys	Tyr	Ile	Gly	Ala	Gly	Asp	Glu	Lys	Arg	Ser	Asp	Ser	Ile	Ser		355	360	365	
Ile	Cys	Thr	Thr	Ser	Asp	Asp	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ile	Glu	370	375	380	
His	Ser	Ser	Glu	Ser	Asp	Asn	Ser	Val	Leu	Glu	Ile	Pro	Asp	Ala	Phe	385	390	395	400
Asp	Arg	Thr	Glu	Asn	Met	Leu	Ser	Met	Gln	Lys	Asn	Glu	Lys	Ile	Lys	405	410		415
Tyr	Ser	Arg	Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys	420	425	430	
Pro	Leu	Ile	Ser	Asn	Ser	His	Thr	Asp	His	Leu	Met	Gly	Cys	Thr	Lys	435	440	445	
Ser	Ala	Glu	Pro	Gly	Thr	Glu	Thr	Ser	Gln	Val	Asn	Leu	Ser	Asp	Leu	450	455	460	
Lys	Ala	Ser	Thr	Leu	Val	His	Lys	Pro	Gln	Ser	Asp	Phe	Thr	Asn	Asp	465	470	475	480
Ala	Leu	Ser	Pro	Lys	Phe	Asn	Leu	Ser	Ser	Ile	Ser	Ser	Glu	Asn		485	490	495	
Ser	Leu	Ile	Lys	Gly	Gly	Ala	Ala	Asn	Gln	Ala	Leu	Leu	His	Ser	Lys	500	505	510	
Ser	Lys	Gln	Pro	Lys	Phe	Arg	Ser	Ile	Lys	Cys	Lys	His	Lys	Glu	Asn	515	520	525	
Pro	Val	Met	Ala	Glu	Pro	Pro	Val	Ile	Asn	Glu	Glu	Cys	Ser	Leu	Lys	530	535	540	

Cys	Cys	Ser	Ser	Asp	Thr	Lys	Gly	Ser	Pro	Leu	Ala	Ser	Ile	Ser	Lys
545					550					555					560
Ser	Gly	Lys	Val	Asp	Gly	Leu	Lys	Leu	Leu	Asn	Asn	Met	His	Glu	Lys
				565					570					575	
Thr	Arg	Asp	Ser	Ser	Asp	Ile	Glu	Thr	Ala	Val	Val	Lys	His	Val	Leu
			580					585					590		
Ser	Glu	Leu	Lys	Glu	Leu	Ser	Tyr	Arg	Ser	Leu	Gly	Glu	Asp	Val	Ser
	595						600					605			
Asp	Ser	Gly	Thr	Ser	Lys	Pro	Ser	Lys	Pro	Leu	Leu	Phe	Ser	Ser	Ala
	610					615					620				
Ser	Ser	Gln	Asn	His	Ile	Pro	Ile	Glu	Pro	Asp	Tyr	Lys	Phe	Ser	Thr
625					630					635					640
Leu	Leu	Met	Met	Leu	Lys	Asp	Met	His	Asp	Ser	Lys	Thr	Lys	Glu	Gln
				645					650					655	
Arg	Leu	Met	Thr	Ala	Gln	Asn	Leu	Val	Ser	Tyr	Arg	Ser	Pro	Gly	Arg
			660					665					670		
Gly	Asp	Cys	Ser	Thr	Asn	Ser	Pro	Val	Gly	Val	Ser	Lys	Val	Leu	Val
	675						680					685			
Ser	Gly	Gly	Ser	Thr	His	Asn	Ser	Glu	Lys	Lys	Gly	Asp	Gly	Thr	Gln
	690					695					700				
Asn	Ser	Ala	Asn	Pro	Ser	Pro	Ser	Gly	Gly	Asp	Ser	Ala	Leu	Ser	Gly
705					710					715					720
Glu	Leu	Ser	Ala	Ser	Leu	Pro	Gly	Leu	Leu	Ser	Asp	Lys	Arg	Asp	Leu
				725					730					735	
Pro	Ala	Ser	Gly	Lys	Ser	Arg	Ser	Asp	Cys	Val	Thr	Arg	Arg	Asn	Cys
			740					745					750		
Gly	Arg	Ser	Lys	Pro	Ser	Ser	Lys	Leu	Arg	Asp	Ala	Phe	Ser	Ala	Gln
	755						760					765			
Met	Val	Lys	Asn	Thr	Val	Asn	Arg	Lys	Ala	Leu	Lys	Thr	Glu	Arg	Lys
	770					775					780				
Arg	Lys	Leu	Asn	Gln	Leu	Pro	Ser	Val	Thr	Leu	Asp	Ala	Val	Leu	Gln
785					790					795					800
Gly	Asp	Arg	Glu	Arg	Gly	Gly	Ser	Leu	Arg	Gly	Gly	Ala	Glu	Asp	Pro
				805					810					815	
Ser	Lys	Glu	Asp	Pro	Leu	Gln	Ile	Met	Gly	His	Leu	Thr	Ser	Glu	Asp
			820					825					830		
Gly	Asp	His	Phe	Ser	Asp	Val	His	Phe	Asp	Ser	Lys	Val	Lys	Gln	Ser
	835						840					845			
Asp	Pro	Gly	Lys	Ile	Ser	Glu	Lys	Gly	Leu	Ser	Phe	Glu	Asn	Gly	Lys
	850					855					860				
Gly	Pro	Glu	Leu	Asp	Ser	Val	Met	Asn	Ser	Glu	Asn	Asp	Glu	Leu	Asn
865					870					875					880
Gly	Val	Asn	Gln	Val	Val	Pro	Lys	Lys	Arg	Trp	Gln	Arg	Leu	Asn	Gln
				885					890					895	
Arg	Arg	Thr	Lys	Pro	Arg	Lys	Arg	Met	Asn	Arg	Phe	Lys	Glu	Lys	Glu
			900					905					910		
Asn	Ser	Glu	Cys	Ala	Phe	Arg	Val	Leu	Leu	Pro	Ser	Asp	Pro	Val	Gln
			915				920					925			
Glu	Gly	Arg	Asp	Glu	Phe	Pro	Glu	His	Arg	Thr	Pro	Ser	Ala	Ser	Ile
	930					935					940				
Leu	Glu	Glu	Pro	Leu	Thr	Glu	Gln	Asn	His	Ala	Asp	Cys	Leu	Asp	Ser
945					950					955					960
Ala	Gly	Pro	Arg	Leu	Asn	Val	Cys	Asp	Lys	Ser	Ser	Ala	Ser	Ile	Gly
				965					970					975	
Asp	Met	Glu	Lys	Glu	Pro	Gly	Ile	Pro	Ser	Leu	Thr	Pro	Gln	Ala	Glu
			980					985					990		
Leu	Pro	Glu	Pro	Ala	Val	Arg	Ser	Glu	Lys	Lys	Arg	Leu	Arg	Lys	Pro
			995				1000					1005			
Ser	Lys	Trp	Leu	Leu	Glu	Tyr	Thr	Glu	Glu	Tyr	Asp	Gln	Ile	Phe	Ala
	1010					1015					1020				

Pro Lys Lys Lys Gln Lys Lys Val Gln Glu Gln Val His Lys Val Ser	1025	1030	1035	1040
Ser Arg Cys Glu Glu Glu Ser Leu Leu Ala Arg Gly Arg Ser Ser Ala		1045	1050	1055
Gln Asn Lys Gln Val Asp Glu Asn Ser Leu Ile Ser Thr Lys Glu Glu	1060		1065	1070
Pro Pro Val Leu Glu Arg Glu Ala Pro Phe Leu Glu Gly Pro Leu Ala	1075	1080		1085
Gln Ser Glu Leu Gly Gly Gly His Ala Glu Leu Pro Gln Leu Thr Leu	1090	1095	1100	
Ser Val Pro Val Ala Pro Glu Val Ser Pro Arg Pro Ala Leu Glu Ser	1105	1110	1115	1120
Glu Glu Leu Leu Val Lys Thr Pro Gly Asn Tyr Glu Ser Lys Arg Gln		1125	1130	1135
Arg Lys Pro Thr Lys Lys Leu Leu Glu Ser Asn Asp Leu Asp Pro Gly	1140		1145	1150
Phe Met Pro Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu	1155	1160		1165
Ala Gly His Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr	1170	1175	1180	
Ser Lys Asp Phe Gly Gly Gly Thr Thr Lys Ile Phe Asp Lys Pro Arg	1185	1190	1195	1200
Lys Arg Lys Arg Gln Arg His Ala Ala Lys Met Gln Cys Lys Lys		1205	1210	1215
Val Lys Asn Asp Asp Ser Ser Lys Glu Ile Pro Gly Ser Glu Gly Glu	1220		1225	1230
Leu Met Pro His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu	1235	1240		1245
Gly Val Glu His Asp Pro Gly Met Pro Ala Ser Lys Lys Met Gln Gly	1250	1255	1260	
Glu Arg Gly Gly Gly Ala Ala Leu Lys Glu Asn Val Cys Gln Asn Cys	1265	1270	1275	1280
Glu Lys Leu Gly Glu Leu Leu Leu Cys Glu Ala Gln Cys Cys Gly Ala		1285	1290	1295
Phe His Leu Glu Cys Leu Gly Leu Thr Glu Met Pro Arg Gly Lys Phe	1300		1305	1310
Ile Cys Asn Glu Cys Arg Thr Gly Ile His Thr Cys Phe Val Cys Lys	1315	1320		1325
Gln Ser Gly Glu Asp Val Lys Arg Cys Leu Leu Pro Leu Cys Gly Lys	1330	1335	1340	
Phe Tyr His Glu Glu Cys Val Gln Lys Tyr Pro Pro Thr Val Met Gln	1345	1350	1355	1360
Asn Lys Gly Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala		1365	1370	1375
Ala Asn Pro Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys	1380	1385		1390
Val Arg Cys Pro Val Ala Tyr His Ala Asn Asp Phe Cys Leu Ala Ala	1395	1400		1405
Gly Ser Lys Ile Leu Ala Ser Asn Ser Ile Ile Cys Pro Asn His Phe	1410	1415	1420	
Thr Pro Arg Arg Gly Cys Arg Asn His Glu His Val Asn Val Ser Trp	1425	1430	1435	1440
Cys Phe Val Cys Ser Glu Gly Gly Ser Leu Leu Cys Cys Asp Ser Cys		1445	1450	1455
Pro Ala Ala Phe His Arg Glu Cys Leu Asn Ile Asp Ile Pro Glu Gly	1460	1465		1470
Asn Trp Tyr Cys Asn Asp Cys Lys Ala Gly Lys Lys Pro His Tyr Arg	1475	1480	1485	
Glu Ile Val Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu	1490	1495	1500	

Ile Cys His Pro Arg Ala Val Pro Ser Asn Ile Asp Lys Met Arg His	1505	1510	1515	1520
Asp Val Gly Glu Phe Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu		1525	1530	1535
Trp Thr His Gln Ala Arg Val Phe Pro Tyr Met Glu Gly Asp Val Ser		1540	1545	1550
Ser Lys Asp Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala	1555		1560	1565
Leu Gln Glu Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu	1570	1575	1580	
Leu Arg Gln Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro	1585	1590	1595	1600
Tyr Lys His Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe		1605	1610	1615
Thr Ala Asp Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp		1620	1625	1630
Glu Asn Pro Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu	1635		1640	1645
Tyr Glu Cys His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn	1650	1655	1660	
Gln Cys Phe Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr	1665	1670	1675	1680
Leu Gln Arg Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly		1685	1690	1695
Glu Phe Val Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys		1700	1705	1710
Arg Ala Arg Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr	1715	1720		1725
Met Leu Thr Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly	1730	1735	1740	
Asn Tyr Ala Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr	1745	1750	1755	1760
Gln Lys Trp Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu		1765	1770	1775
Ser Asp Ile Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu	1780		1785	1790
Cys Leu Gly Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys	1795	1800		1805
Ser Gly Phe Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu	1810	1815	1820	
Glu Lys Ser Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr	1825	1830	1835	1840
Gln Gly Glu Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly		1845	1850	1855
Asp Ala Gly Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val	1860	1865		1870
Tyr His Ala Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp	1875	1880	1885	
Glu Cys Pro Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser	1890	1895	1900	
Phe Cys Glu Met Cys Pro Ser Ser Phe Cys Lys Gln His Arg Glu Gly	1905	1910	1915	1920
Met Leu Phe Ile Ser Lys Leu Asp Gly Arg Leu Ser Cys Thr Glu His		1925	1930	1935
Asp Pro Cys Gly Pro Asn Pro Leu Glu Pro Gly Glu Ile Arg Glu Tyr	1940	1945	1950	
Val Pro Pro Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala	1955	1960	1965	
Glu Gln Ser Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys	1970	1975	1980	

Pro Pro Ala Asp Thr Asn Gln Met Leu Ser Leu Ser Lys Lys Ala Leu
1985 1990 1995 2000
Ala Gly Thr Cys Gln Arg Pro Leu Leu Pro Glu Arg Pro Leu Glu Arg
2005 2010 2015
Thr Asp Ser Arg Pro Gln Pro Leu Asp Lys Val Arg Asp Leu Ala Gly
2020 2025 2030
Ser Gly Thr Lys Ser Gln Ser Leu Val Ser Ser Gln Arg Pro Leu Asp
2035 2040 2045
Arg Pro Pro Ala Val Ala Gly Pro Arg Pro Gln Leu Ser Asp Lys Pro
2050 2055 2060
Ser Pro Val Thr Ser Pro Ser Ser Pro Ser Val Arg Ser Gln Pro
2065 2070 2075 2080
Leu Glu Arg Pro Leu Gly Thr Ala Asp Pro Arg Leu Asp Lys Ser Ile
2085 2090 2095
Gly Ala Ala Ser Pro Arg Pro Gln Ser Leu Glu Lys Thr Ser Val Pro
2100 2105 2110
Thr Gly Leu Arg Leu Pro Pro Pro Asp Arg Leu Leu Ile Thr Ser Ser
2115 2120 2125
Pro Lys Pro Gln Thr Ser Asp Arg Pro Thr Asp Lys Pro His Ala Ser
2130 2135 2140
Leu Ser Gln Arg Leu Pro Pro Pro Glu Lys Val Leu Ser Ala Val Val
2145 2150 2155 2160
Gln Thr Leu Val Ala Lys Glu Lys Ala Leu Arg Pro Val Asp Gln Asn
2165 2170 2175
Thr Gln Ser Lys Asn Arg Ala Ala Leu Val Met Asp Leu Ile Asp Leu
2180 2185 2190
Thr Pro Arg Gln Lys Glu Arg Ala Ala Ser Pro His Gln Val Thr Pro
2195 2200 2205
Gln Ala Asp Glu Lys Met Pro Val Leu Glu Ser Ser Ser Trp Pro Ala
2210 2215 2220
Ser Lys Gly Leu Gly His Met Pro Arg Ala Val Glu Lys Gly Cys Val
2225 2230 2235 2240
Ser Asp Pro Leu Gln Thr Ser Gly Lys Ala Ala Ala Pro Ser Glu Asp
2245 2250 2255
Pro Trp Gln Ala Val Lys Ser Leu Thr Gln Ala Arg Leu Leu Ser Gln
2260 2265 2270
Pro Pro Ala Lys Ala Phe Leu Tyr Glu Pro Thr Thr Gln Ala Ser Gly
2275 2280 2285
Arg Ala Ser Ala Gly Ala Glu Gln Thr Pro Gly Pro Leu Ser Gln Ser
2290 2295 2300
Pro Gly Leu Val Lys Gln Ala Lys Gln Met Val Gly Gly Gln Gln Leu
2305 2310 2315 2320
Pro Ala Leu Ala Ala Lys Ser Gly Gln Ser Phe Arg Ser Leu Gly Lys
2325 2330 2335
Ala Pro Ala Ser Leu Pro Thr Glu Glu Lys Lys Leu Val Thr Thr Glu
2340 2345 2350
Gln Ser Pro Trp Ala Leu Gly Lys Ala Ser Ser Arg Ala Gly Leu Trp
2355 2360 2365
Pro Ile Val Ala Gly Gln Thr Leu Ala Gln Ser Cys Trp Ser Ala Gly
2370 2375 2380
Ser Thr Gln Thr Leu Ala Gln Thr Cys Trp Ser Leu Gly Arg Gly Gln
2385 2390 2395 2400
Asp Pro Lys Pro Glu Gln Asn Thr Leu Pro Ala Leu Asn Gln Ala Pro
2405 2410 2415
Ser Ser His Lys Cys Ala Glu Ser Glu Gln Lys
2420 2425

<210> 35

<211> 7707

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 35

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cagccctttc	ggatgatcca	gattccagta	ccagtacatt	aggaaacatg	ctagaattac	180
ctggaacttc	atcatcatct	acttcacagg	aattgccatt	ttgtcaacct	aagaaaaagt	240
ctacgccact	gaagtatgaa	gttgagatc	tcatctgggc	aaaattcaag	agacgcccac	300
ggtggccctg	caggatttgt	tctgatccgt	tgattaacac	acattcaaaa	atgaaagtgt	360
ccaaccggag	gccctatcgg	cagtactacg	tggaggcttt	tggagatcct	tctgagagag	420
cctgggtggc	tggaaaagca	atcgatcatg	ttgaaggcag	acatcaattc	gaagagctac	480
ctgtccttag	gagaagaggg	aaacagaaaag	aaaaaggata	taggcataag	gttcctcaga	540
aaatttttgag	taaatgggaa	gccagtgttg	gacttgcaga	acagtatgat	gttcccaagg	600
ggtcaaagaa	ccgaaaatgt	attcctgggt	caatcaagtt	ggacagtga	gaagatatgc	660
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acactgcaaa	gaaagaattt	gagacttcaa	atgggtgactc	tttattgggc	ttgcctgagg	1080
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taaaactact	gaacaatatg	catgagaaaa	ccagggtattc	aagtgcacata	gaaacagcag	1860
tggtagaaca	tgttttatcc	gagttgaagg	aactctctta	cagatccctta	ggtgaggatg	1920
tcagtgactc	tggaaacatca	aagccatcaa	aaccattact	tttctcttct	gcttctagtc	1980
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<210> 36

<211> 2696

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 36

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Gly Asn Gly Gln Ser Asn Phe Ser Glu Pro Leu Asn Gly Cys Thr Met
          35          40          45
Gln Leu Ser Thr Val Ser Gly Thr Ser Gln Asn Ala Tyr Gly Gln Asp
          50          55          60
Ser Pro Ser Cys Tyr Ile Pro Leu Arg Arg Leu Gln Asp Leu Ala Ser
65          70          75          80
Met Ile Asn Val Glu Tyr Leu Asn Gly Ser Ala Asp Gly Ser Glu Ser
          85          90          95
Phe Gln Asp Pro Glu Lys Ser Asp Ser Arg Ala Gln Thr Pro Ile Val
          100          105          110
Cys Thr Ser Leu Ser Pro Gly Gly Pro Thr Ala Leu Ala Met Lys Gln
          115          120          125
Glu Pro Ser Cys Asn Asn Ser Pro Glu Leu Gln Val Lys Val Thr Lys
          130          135          140
Thr Ile Lys Asn Gly Phe Leu His Phe Glu Asn Phe Thr Cys Val Asp
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Asp Ala Asp Val Asp Ser Glu Met Asp Pro Glu Gln Pro Val Thr Glu
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Asp Glu Ser Ile Glu Glu Ile Phe Glu Glu Thr Gln Thr Asn Ala Thr
          180          185          190
Cys Asn Tyr Glu Thr Lys Ser Glu Asn Gly Val Lys Val Ala Met Gly
          195          200          205
Ser Glu Gln Asp Ser Thr Pro Glu Ser Arg His Gly Ala Val Lys Ser
          210          215          220
Pro Phe Leu Pro Leu Ala Pro Gln Thr Glu Thr Gln Lys Asn Lys Gln
225          230          235          240
Arg Asn Glu Val Asp Gly Ser Asn Glu Lys Ala Ala Leu Leu Pro Ala
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<210> 38

<211> 1784

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 38

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Arg Leu Leu Glu Glu Asp Thr Pro Arg Tyr Met Arg Ala Ser Asp Pro
      35             40             45
Ala Ser Pro His Ile Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp
      50             55             60
Ser Ser Leu Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser
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Arg	Arg	Gln	Leu	Ala	Glu	Lys	Tyr	Gly	Leu	Thr	Leu	Asp	Pro	Glu	Ala	115	120	125
Asp	Ser	Glu	Tyr	Leu	Ser	Arg	Tyr	Thr	Lys	Ser	Arg	Lys	Glu	Pro	Asp	130	135	140
Ala	Val	Glu	Lys	Arg	Gly	Gly	Lys	Ser	Asp	Lys	Gln	Glu	Glu	Ser	Ser	145	150	155
Arg	Asp	Ala	Ser	Ser	Leu	Tyr	Pro	Gly	Thr	Glu	Thr	Met	Gly	Leu	Arg	165	170	175
Thr	Cys	Ala	Gly	Glu	Ser	Lys	Asp	Tyr	Ala	Leu	His	Ala	Gly	Asp	Gly	180	185	190
Ser	Ser	Asp	Pro	Glu	Val	Leu	Leu	Asn	Ile	Glu	Asn	Gln	Arg	Arg	Gly	195	200	205
Gln	Glu	Leu	Ser	Ala	Thr	Arg	Gln	Ala	His	Asp	Leu	Ser	Pro	Ala	Ala	210	215	220
Glu	Ser	Ser	Ser	Thr	Phe	Ser	Phe	Ser	Gly	Arg	Asp	Ser	Ser	Phe	Thr	225	230	235
Glu	Val	Pro	Arg	Ser	Pro	Lys	His	Ala	His	Ser	Ser	Ser	Leu	Gln	Gln	245	250	255
Ala	Ala	Ser	Arg	Ser	Pro	Ser	Phe	Gly	Asp	Pro	Gln	Leu	Ser	Pro	Glu	260	265	270
Ala	Arg	Pro	Arg	Cys	Thr	Ser	His	Ser	Glu	Thr	Pro	Thr	Val	Asp	Asp	275	280	285
Glu	Glu	Lys	Val	Asp	Glu	Arg	Ala	Lys	Leu	Ser	Val	Ala	Ala	Lys	Arg	290	295	300
Leu	Leu	Phe	Arg	Glu	Met	Glu	Lys	Ser	Phe	Asp	Glu	Gln	Asn	Val	Pro	305	310	315
Lys	Arg	Arg	Ser	Arg	Asn	Thr	Ala	Val	Glu	Gln	Arg	Leu	Arg	Arg	Leu	325	330	335
Gln	Asp	Arg	Ser	Leu	Thr	Gln	Pro	Ile	Thr	Thr	Glu	Glu	Val	Val	Ile	340	345	350
Ala	Ala	Thr	Leu	Gln	Ala	Ser	Ala	His	Gln	Lys	Ala	Leu	Ala	Lys	Asp	355	360	365
Gln	Thr	Asn	Glu	Gly	Lys	Glu	Leu	Ala	Glu	Gln	Gly	Glu	Pro	Asp	Ser	370	375	380
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Glu	Val	Glu	Gln	Val	Gln	Ser	Gly	Lys	Leu	Ile	Pro	Phe	Ser	Pro	Ala	435	440	445
Val	Asn	Thr	Ser	Val	Ser	Thr	Val	Ala	Ser	Thr	Val	Ala	Pro	Met	Tyr	450	455	460
Ala	Gly	Asp	Leu	Arg	Thr	Lys	Pro	Pro	Leu	Asp	His	Asn	Ala	Ser	Ala	465	470	475
Thr	Asp	Tyr	Lys	Phe	Ser	Ser	Ser	Ile	Glu	Asn	Ser	Asp	Ser	Pro	Val	485	490	495
Arg	Ser	Ile	Leu	Lys	Ser	Gln	Ala	Trp	Gln	Pro	Leu	Val	Glu	Gly	Ser	500	505	510
Glu	Asn	Lys	Gly	Met	Leu	Arg	Glu	Tyr	Gly	Glu	Thr	Glu	Ser	Lys	Arg	515	520	525
Ala	Leu	Thr	Gly	Arg	Asp	Ser	Gly	Met	Glu	Lys	Tyr	Gly	Ser	Phe	Glu	530	535	540
Glu	Ala	Glu	Ala	Ser	Tyr	Pro	Ile	Leu	Asn	Arg	Ala	Arg	Glu	Gly	Asp	545	550	555

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Phe	Ser	Leu	Arg	Ala	Ala	Glu	Phe	Gly	Glu	Pro	Thr	Ser	Glu	Gln	Thr		
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Trp	Lys	Pro	Gln	Asp	Ser	Ser	Glu	Gln	Pro	Gln	Glu	Lys	Leu	Cys	Lys		
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Asn	Pro	Cys	Ala	Met	Phe	Ala	Ala	Gly	Glu	Ile	Lys	Thr	Pro	Thr	Gly		
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Glu	Gly	Leu	Leu	Asp	Ser	Pro	Ser	Lys	Thr	Met	Ser	Ile	Lys	Glu	Arg		
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Ser	Arg	Arg	Gln	Glu	Gly	Gly	Lys	Ala	Pro	Ala	Ser	Ser	Leu	His	Thr		
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Gln	Glu	Ala	Gly	Arg	Ser	Leu	Ile	Lys	Lys	Arg	Val	Thr	Glu	Ser	Arg		
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Met	Gln	Leu	Glu	Ser	Asp	Leu	Lys	Leu	Asp	Arg	Leu	Glu	Thr	Phe	Leu		
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Arg	Arg	Leu	Asn	Asn	Lys	Val	Gly	Gly	Met	His	Glu	Thr	Val	Leu	Thr		
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Thr	Phe	Ala	Lys	Phe	Tyr	Arg	Ser	Val	Asp	Tyr	Asn	Met	Pro	Arg	Ser		
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Ile His Glu Cys Asp Glu Gly Ser Glu Pro Leu Gly Phe Trp Asp Ala
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Gly Asp Phe Ala Ala Thr Glu Phe Val Tyr Pro Ala Arg Ala Pro Ser
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<211> 6719

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 39

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<210> 40

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 40

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Leu	Gln	Ile	Trp	Arg	Val	Glu	Lys	Phe	Asp	Leu	Val	Pro	Val	Pro	Pro
			20					25					30		
Asn	Leu	Tyr	Gly	Asp	Phe	Phe	Thr	Gly	Asp	Ala	Tyr	Val	Ile	Leu	Lys
		35					40					45			
Thr	Val	Gln	Leu	Arg	Asn	Gly	Asn	Leu	Gln	Tyr	Asp	Leu	His	Tyr	Trp
	50					55					60				
Leu	Gly	Asn	Glu	Cys	Ser	Gln	Asp	Glu	Ser	Gly	Ala	Ala	Ala	Ile	Phe
65					70					75				80	
Thr	Val	Gln	Leu	Asp	Asp	Tyr	Leu	Asn	Gly	Arg	Ala	Val	Gln	His	Arg
			85					90						95	

Glu	Val	Gln	Gly	Phe	Glu	Ser	Ser	Thr	Phe	Ser	Gly	Tyr	Phe	Lys	Ser	100	105	110
Gly	Leu	Lys	Tyr	Lys	Lys	Gly	Gly	Val	Ala	Ser	Gly	Phe	Lys	His	Val	115	120	125
Val	Pro	Asn	Glu	Val	Val	Val	Gln	Arg	Leu	Phe	Gln	Val	Lys	Gly	Arg	130	135	140
Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Val	Ser	Trp	Asp	Ser	Phe	Asn	145	150	155
Asn	Gly	Asp	Cys	Phe	Ile	Leu	Asp	Leu	Gly	Asn	Asn	Ile	Tyr	Gln	Trp	165	170	175
Cys	Gly	Ser	Gly	Ser	Asn	Lys	Phe	Glu	Arg	Leu	Lys	Ala	Thr	Gln	Val	180	185	190
Ser	Lys	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Ser	Gly	Arg	Ala	Gln	Val	His	195	200	205
Val	Ser	Glu	Glu	Glu	Thr	Glu	Pro	Glu	Ala	Met	Leu	Gln	Val	Leu	Gly	210	215	220
Pro	Lys	Pro	Ala	Leu	Pro	Glu	Gly	Thr	Glu	Asp	Thr	Ala	Lys	Glu	Asp	225	230	235
Ala	Ala	Asn	Arg	Lys	Leu	Ala	Lys	Leu	Tyr	Lys	Val	Ser	Asn	Gly	Ala	245	250	255
Gly	Ser	Met	Ser	Val	Ser	Leu	Val	Ala	Asp	Glu	Asn	Pro	Phe	Ala	Gln	260	265	270
Gly	Pro	Leu	Arg	Ser	Glu	Asp	Cys	Phe	Ile	Leu	Asp	His	Gly	Arg	Asp	275	280	285
Gly	Lys	Ile	Phe	Val	Trp	Lys	Gly	Lys	Gln	Ala	Asn	Met	Glu	Glu	Arg	290	295	300
Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Ser	Lys	Met	Gln	Tyr	305	310	315
Pro	Arg	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly	Glu	Thr	Pro	325	330	335
Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp	Gln	Thr	Asp	340	345	350
Gly	Pro	Gly	Leu	Gly	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn	Val	Glu	Arg	355	360	365
Val	Pro	Phe	Asp	Ala	Gly	Thr	Leu	His	Thr	Ser	Thr	Ala	Met	Ala	Ala	370	375	380
Gln	His	Gly	Met	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln	Ile	Trp	Arg		385	390	395
Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr	Tyr	Gly	Gln	405	410	415
Phe	Tyr	Gly	Gly	Asp	Ser	Tyr	Ile	Ile	Leu	Tyr	Asn	Tyr	Arg	His	Gly	420	425	430
Gly	Arg	Gln	Gly	Gln	Ile	Ile	Tyr	Asn	Trp	Gln	Gly	Ala	Gln	Ser	Thr	435	440	445
Gln	Asp	Glu	Val	Ala	Ala	Ser	Ala	Ile	Leu	Thr	Ala	Gln	Leu	Asp	Glu	450	455	460
Glu	Leu	Gly	Gly	Thr	Pro	Val	Gln	Ser	Arg	Val	Val	Gln	Gly	Lys	Glu	465	470	475
Pro	Ala	His	Leu	Met	Ser	Leu	Phe	Gly	Gly	Lys	Pro	Met	Ile	Ile	Tyr	485	490	495
Lys	Gly	Gly	Thr	Ser	Arg	Asp	Gly	Gly	Gln	Thr	Ala	Pro	Ala	Ser	Ile	500	505	510
Arg	Leu	Phe	Gln	Val	Arg	Ala	Ser	Ser	Ser	Gly	Ala	Thr	Arg	Ala	Val	515	520	525
Glu	Val	Met	Pro	Lys	Ser	Gly	Ala	Leu	Asn	Ser	Asn	Asp	Ala	Phe	Val	530	535	540
Leu	Lys	Thr	Pro	Ser	Ala	Ala	Tyr	Leu	Trp	Val	Gly	Ala	Gly	Ala	Ser	545	550	555
Glu	Ala	Glu	Lys	Thr	Ala	Ala	Gln	Glu	Leu	Leu	Lys	Val	Leu	Arg	Ser	565	570	575


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ggcgggaaga cgtcctaccg cacatccccc aggcttaagg acaagaagat ggatgcccat 1860
cctcctcgac tctttgcctg ctccaacagg atcggacgct ttgtgatcga agaggttcct 1920
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<210> 42

<211> 928

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 42

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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
 1          5          10          15
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
          20          25          30
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
          35          40          45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
          50          55          60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
          65          70          75          80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
          85          90          95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
          100          105          110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
          115          120          125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
          130          135          140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
          145          150          155          160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
          165          170          175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
          180          185          190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
          195          200          205
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
          210          215          220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
          225          230          235          240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
          245          250          255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
          260          265          270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
          275          280          285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
          290          295          300

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Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315	320
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395	400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430	
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475	480
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	485	490	495	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	500	505	510	
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	515	520	525	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	530	535	540	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	545	550	555	560
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	565	570	575	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	580	585	590	
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	595	600	605	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	610	615	620	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	625	630	635	640
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	645	650	655	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	660	665	670	
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	675	680	685	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	690	695	700	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	705	710	715	720
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	725	730	735	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	740	745	750	
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	755	760	765	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	770	775	780	

Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro
785					790				795					800	
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser
			805					810						815	
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
			820					825					830		
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
		835					840					845			
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
	850					855					860				
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
			885					890						895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
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<210> 43

<211> 2994

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 43

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aaaaaggaac	tgtggggaat	ctgtatcttt	attgcagcag	ttgacctaga	tgagatgtcg	480
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gaaaatcttt	ctaaacgata	cgaagaaatt	tatcttataa	ataaagatct	agatgcaaga	1140
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ccatggattc	tgaatgtgct	taatttataa	gcctttgatt	tttataaaag	gatcgaaagt	1740
tttatcaaag	cagaaggcaa	cttgacaaga	gaaatgataa	aacattttaga	acgatgtgaa	1800
catcgaatca	tggaaatccct	tgcattggctc	tcagattcac	ctttatttga	tcttattaaa	1860
caatcaaagg	accgagaagg	accaactgat	caccttgaat	ctgcttgctc	tcttaattct	1920

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cctctccaga ataatcacac tgcagcagat atgtatcttt ctctgtgaag atctccaaag 1980
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ctacgctttg atattgaagg atcagatgaa gcagatggaa gtaaaccatct cccaggagag 2820
tccaaatttc agcagaaact ggcagaaatg acttctactc gaacacgaat gcaaaagcag 2880
aaaatgaatg atagcatgga tacctcaaac aaggaagaga aatgaggatc tcaggacctt 2940
ggtggacact gtgtacacct ctggattcat tgtctctcac agatgtgact gtat 2994

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<210> 44

<211> 782

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 44

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Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
 1           5           10          15
Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
 20          25          30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
 35          40          45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
 50          55          60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
 65          70          75          80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
 85          90          95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
100         105         110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
115         120         125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
130         135         140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145         150         155         160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
165         170         175
Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
180         185         190
Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
195         200         205
Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
210         215         220
His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225         230         235         240

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Thr	Gln	Val	Ser	Lys	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Ser	Gly	Arg	Ala		
				245					250						255		
Arg	Val	His	Val	Ser	Glu	Glu	Gly	Thr	Glu	Pro	Glu	Ala	Met	Leu	Gln		
			260					265					270				
Val	Leu	Gly	Pro	Lys	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Glu	Asp	Thr	Ala		
		275					280					285					
Lys	Glu	Asp	Ala	Ala	Asn	Arg	Lys	Leu	Ala	Lys	Leu	Tyr	Lys	Val	Ser		
	290				295						300						
Asn	Gly	Ala	Gly	Thr	Met	Ser	Val	Ser	Leu	Val	Ala	Asp	Glu	Asn	Pro		
305					310					315					320		
Phe	Ala	Gln	Gly	Ala	Leu	Lys	Ser	Glu	Asp	Cys	Phe	Ile	Leu	Asp	His		
				325					330						335		
Gly	Lys	Asp	Gly	Lys	Ile	Phe	Val	Trp	Lys	Gly	Lys	Gln	Ala	Asn	Thr		
			340					345						350			
Glu	Glu	Arg	Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Thr	Lys		
								360						365			
Met	Asp	Tyr	Pro	Lys	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly		
	370					375					380						
Glu	Thr	Pro	Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp		
385					390					395					400		
Gln	Thr	Asp	Gly	Leu	Gly	Leu	Ser	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn		
				405					410						415		
Val	Glu	Arg	Val	Pro	Phe	Asp	Ala	Ala	Thr	Leu	His	Thr	Ser	Thr	Ala		
				420				425						430			
Met	Ala	Ala	Gln	His	Gly	Met	Asp	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln		
							440						445				
Ile	Trp	Arg	Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr		
	450					455					460						
Tyr	Gly	Gln	Phe	Tyr	Gly	Gly	Asp	Ser	Tyr	Ile	Ile	Leu	Tyr	Asn	Tyr		
465					470					475					480		
Arg	His	Gly	Gly	Arg	Gln	Gly	Gln	Ile	Ile	Tyr	Asn	Trp	Gln	Gly	Ala		
				485					490						495		
Gln	Ser	Thr	Gln	Asp	Glu	Val	Ala	Ala	Ser	Ala	Ile	Leu	Thr	Ala	Gln		
				500					505					510			
Leu	Asp	Glu	Glu	Leu	Gly	Gly	Thr	Pro	Val	Gln	Ser	Arg	Val	Val	Gln		
				515			520						525				
Gly	Lys	Glu	Pro	Ala	His	Leu	Met	Ser	Leu	Phe	Gly	Gly	Lys	Pro	Met		
	530					535					540						
Ile	Ile	Tyr	Lys	Gly	Gly	Thr	Ser	Arg	Glu	Gly	Gly	Gln	Thr	Ala	Pro		
545					550					555					560		
Ala	Ser	Thr	Arg	Leu	Phe	Gln	Val	Arg	Ala	Asn	Ser	Ala	Gly	Ala	Thr		
				565					570						575		
Arg	Ala	Val	Glu	Val	Leu	Pro	Lys	Ala	Gly	Ala	Leu	Asn	Ser	Asn	Asp		
				580				585						590			
Ala	Phe	Val	Leu	Lys	Thr	Pro	Ser	Ala	Ala	Tyr	Leu	Trp	Val	Gly	Thr		
		595					600						605				
Gly	Ala	Ser	Glu	Ala	Glu	Lys	Thr	Gly	Ala	Gln	Glu	Leu	Leu	Arg	Val		
	610					615					620						
Leu	Arg	Ala	Gln	Pro	Val	Gln	Val	Ala	Glu	Gly	Ser	Glu	Pro	Asp	Gly		
625					630					635					640		
Phe	Trp	Glu	Ala	Leu	Gly	Gly	Lys	Ala	Ala	Tyr	Arg	Thr	Ser	Pro	Arg		
				645					650						655		
Leu	Lys	Asp	Lys	Lys	Met	Asp	Ala	His	Pro	Pro	Arg	Leu	Phe	Ala	Cys		
			660					665						670			
Ser	Asn	Lys	Ile	Gly	Arg	Phe	Val	Ile	Glu	Glu	Val	Pro	Gly	Glu	Leu		
		675					680						685				
Met	Gln	Glu	Asp	Leu	Ala	Thr	Asp	Asp	Val	Met	Leu	Leu	Asp	Thr	Trp		
	690					695						700					
Asp	Gln	Val	Phe	Val	Trp	Val	Gly	Lys	Asp	Ser	Gln	Glu	Glu	Glu	Lys		
705					710						715				720		

Thr	Glu	Ala	Leu	Thr	Ser	Ala	Lys	Arg	Tyr	Ile	Glu	Thr	Asp	Pro	Ala
				725					730					735	
Asn	Arg	Asp	Arg	Arg	Thr	Pro	Ile	Thr	Val	Val	Lys	Gln	Gly	Phe	Glu
			740					745					750		
Pro	Pro	Ser	Phe	Val	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Asp	Asp	Tyr	Trp
		755					760				765				
Ser	Val	Asp	Pro	Leu	Asp	Arg	Ala	Met	Ala	Glu	Leu	Ala	Ala		
	770					775					780				

<210> 45

<211> 2663

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 45

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cgccccagg	gcggtgccc	gaggcgggc	ccaacagcat	ggtggtggaa	caccccgagt	180
tcctcaaggc	agggaggag	cctggcctgc	agatctggcg	tgtggagaag	ttcgatctgg	240
tgcccgtgcc	caccaacctt	tatggagact	tcttcacggg	cgacgcctac	gtcatcctga	300
agacagtgca	gctgagggaac	ggaaatctgc	agtatgacct	ccactactgg	ctgggcaatg	360
agtgcagcca	ggatgagagc	ggggcgccc	ccatctttac	cgtgcagctg	gatgactacc	420
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gctacttcaa	gtctggcctg	aagtacaaga	aaggaggtgt	ggcatcagga	ttcaagcacg	540
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gtgccaccga	gggacctgtg	tcctgggaga	gcttcaacaa	tggcgactgc	ttcatcctgg	660
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tcaaaacagc	ctctgacttc	atcacaaga	tggactaccc	caagcagact	caggtctcgg	1140
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aaaaaaaaaa aaaaaaaaaa aaa 2663

<210> 46
<211> 1441
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 46
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His Lys Arg Lys Gly Ser Pro Cys Asp Thr Leu Ala Ser Ser Thr Glu
20 25 30
Lys Arg Arg Arg Glu Gln Glu Asn Lys Tyr Leu Glu Glu Leu Ala Glu
35 40 45
Leu Leu Ser Ala Asn Ile Ser Asp Ile Asp Ser Leu Ser Val Lys Pro
50 55 60
Asp Lys Cys Lys Ile Leu Lys Lys Thr Val Asp Gln Ile Gln Leu Met
65 70 75 80
Lys Arg Met Glu Gln Glu Lys Ser Thr Thr Asp Asp Asp Val Gln Lys
85 90 95
Ser Asp Ile Ser Ser Ser Ser Gln Gly Val Ile Glu Lys Glu Ser Leu
100 105 110
Gly Pro Leu Leu Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn
115 120 125
Cys Glu Gly Arg Ile Val Phe Val Ser Glu Asn Val Thr Ser Tyr Leu
130 135 140
Gly Tyr Asn Gln Glu Glu Leu Met Asn Thr Ser Val Tyr Ser Ile Leu
145 150 155 160
His Val Gly Asp His Ala Glu Phe Val Lys Asn Leu Leu Pro Lys Ser
165 170 175
Leu Val Asn Gly Val Pro Trp Pro Gln Glu Ala Thr Arg Arg Asn Ser
180 185 190
His Thr Phe Asn Cys Arg Met Leu Ile His Pro Pro Asp Glu Pro Gly
195 200 205
Thr Glu Asn Gln Glu Ala Cys Gln Arg Tyr Glu Val Met Gln Cys Phe
210 215 220
Thr Val Ser Gln Pro Lys Ser Ile Gln Glu Asp Gly Glu Asp Phe Gln
225 230 235 240
Ser Cys Leu Ile Cys Ile Ala Arg Arg Leu Pro Arg Pro Pro Ala Ile
245 250 255
Thr Gly Val Glu Ser Phe Met Thr Lys Gln Asp Thr Thr Gly Lys Ile
260 265 270
Ile Ser Ile Asp Thr Ser Ser Leu Arg Ala Ala Gly Arg Thr Gly Trp
275 280 285
Glu Asp Leu Val Arg Lys Cys Ile Tyr Ala Phe Phe Gln Pro Gln Gly
290 295 300
Arg Glu Pro Ser Tyr Ala Arg Gln Leu Phe Gln Glu Val Met Thr Arg
305 310 315 320
Gly Thr Ala Ser Ser Pro Ser Tyr Arg Phe Ile Leu Asn Asp Gly Thr
325 330 335
Met Leu Ser Ala His Thr Lys Cys Lys Leu Cys Tyr Pro Gln Ser Pro
340 345 350
Asp Met Gln Pro Phe Ile Met Gly Ile His Ile Ile Asp Arg Glu His
355 360 365

Ser	Gly	Leu	Ser	Pro	Gln	Asp	Asp	Thr	Asn	Ser	Gly	Met	Ser	Ile	Pro	370	375	380
Arg	Val	Asn	Pro	Ser	Val	Asn	Pro	Ser	Ile	Ser	Pro	Ala	His	Gly	Val	385	390	395
Ala	Arg	Ser	Ser	Thr	Leu	Pro	Pro	Ser	Asn	Ser	Asn	Met	Val	Ser	Thr	405	410	415
Arg	Ile	Asn	Arg	Gln	Gln	Ser	Ser	Asp	Leu	His	Ser	Ser	Ser	His	Ser	420	425	430
Asn	Ser	Ser	Asn	Ser	Gln	Gly	Ser	Phe	Gly	Cys	Ser	Pro	Gly	Ser	Gln	435	440	445
Ile	Val	Ala	Asn	Val	Ala	Leu	Asn	Lys	Gly	Gln	Ala	Ser	Ser	Gln	Ser	450	455	460
Ser	Lys	Pro	Ser	Leu	Asn	Leu	Asn	Asn	Pro	Pro	Met	Glu	Gly	Thr	Gly	465	470	475
Ile	Ser	Leu	Ala	Gln	Phe	Met	Ser	Pro	Arg	Arg	Gln	Val	Thr	Ser	Gly	485	490	495
Leu	Ala	Thr	Arg	Pro	Arg	Met	Pro	Asn	Asn	Ser	Phe	Pro	Pro	Asn	Ile	500	505	510
Ser	Thr	Leu	Ser	Ser	Pro	Val	Gly	Met	Thr	Ser	Ser	Ala	Cys	Asn	Asn	515	520	525
Asn	Asn	Arg	Ser	Tyr	Ser	Asn	Ile	Pro	Val	Thr	Ser	Leu	Gln	Gly	Met	530	535	540
Asn	Glu	Gly	Pro	Asn	Asn	Ser	Val	Gly	Phe	Ser	Ala	Ser	Ser	Pro	Val	545	550	555
Leu	Arg	Gln	Met	Ser	Ser	Gln	Asn	Ser	Pro	Ser	Arg	Leu	Asn	Ile	Gln	565	570	575
Pro	Ala	Lys	Ala	Glu	Ser	Lys	Asp	Asn	Lys	Glu	Ile	Ala	Ser	Thr	Leu	580	585	590
Asn	Glu	Met	Ile	Gln	Ser	Asp	Asn	Ser	Ser	Ser	Asp	Gly	Lys	Pro	Leu	595	600	605
Asp	Ser	Gly	Leu	Leu	His	Asn	Asn	Asp	Arg	Leu	Ser	Asp	Gly	Asp	Ser	610	615	620
Lys	Tyr	Ser	Gln	Thr	Ser	His	Lys	Leu	Val	Gln	Leu	Leu	Thr	Thr	Thr	625	630	635
Ala	Glu	Gln	Gln	Leu	Arg	His	Ala	Asp	Ile	Asp	Thr	Ser	Cys	Lys	Asp	645	650	655
Val	Leu	Ser	Cys	Thr	Gly	Thr	Ser	Asn	Ser	Ala	Ser	Ala	Asn	Ser	Ser	660	665	670
Gly	Gly	Ser	Cys	Pro	Ser	Ser	His	Ser	Ser	Leu	Thr	Ala	Arg	His	Lys	675	680	685
Ile	Leu	His	Arg	Leu	Leu	Gln	Glu	Gly	Ser	Pro	Ser	Asp	Ile	Thr	Thr	690	695	700
Leu	Ser	Val	Glu	Pro	Asp	Lys	Lys	Asp	Ser	Ala	Ser	Thr	Ser	Val	Ser	705	710	715
Val	Thr	Gly	Gln	Val	Gln	Gly	Asn	Ser	Ser	Ile	Lys	Leu	Glu	Leu	Asp	725	730	735
Ala	Ser	Lys	Lys	Lys	Glu	Ser	Lys	Asp	His	Gln	Leu	Leu	Arg	Tyr	Leu	740	745	750
Leu	Asp	Lys	Asp	Glu	Lys	Asp	Leu	Arg	Ser	Thr	Pro	Asn	Leu	Ser	Leu	755	760	765
Asp	Asp	Val	Lys	Val	Lys	Val	Glu	Lys	Lys	Glu	Gln	Met	Asp	Pro	Cys	770	775	780
Asn	Thr	Asn	Pro	Thr	Pro	Met	Thr	Lys	Pro	Thr	Pro	Glu	Glu	Ile	Lys	785	790	795
Leu	Glu	Ala	Gln	Ser	Gln	Phe	Thr	Ala	Asp	Leu	Asp	Gln	Phe	Asp	Gln	805	810	815
Leu	Leu	Pro	Thr	Leu	Glu	Lys	Ala	Ala	Gln	Leu	Pro	Gly	Leu	Cys	Glu	820	825	830

Thr	Asp	Arg	Met	Asp	Gly	Ala	Val	Thr	Ser	Val	Thr	Ile	Lys	Ser	Glu	835	840	845
Ile	Leu	Pro	Ala	Ser	Leu	Gln	Ser	Ala	Thr	Ala	Arg	Pro	Thr	Ser	Arg	850	855	860
Leu	Asn	Arg	Leu	Pro	Glu	Leu	Glu	Leu	Glu	Ala	Ile	Asp	Asn	Gln	Phe	865	870	875
Gly	Gln	Pro	Gly	Thr	Gly	Asp	Gln	Ile	Pro	Trp	Thr	Asn	Asn	Thr	Val	885	890	895
Thr	Ala	Ile	Asn	Gln	Ser	Lys	Ser	Glu	Asp	Gln	Cys	Ile	Ser	Ser	Gln	900	905	910
Leu	Asp	Glu	Leu	Leu	Cys	Pro	Pro	Thr	Thr	Val	Glu	Gly	Arg	Asn	Asp	915	920	925
Glu	Lys	Ala	Leu	Leu	Glu	Gln	Leu	Val	Ser	Phe	Leu	Ser	Gly	Lys	Asp	930	935	940
Glu	Thr	Glu	Leu	Ala	Glu	Leu	Asp	Arg	Ala	Leu	Gly	Ile	Asp	Lys	Leu	945	950	955
Val	Gln	Gly	Gly	Gly	Leu	Asp	Val	Leu	Ser	Glu	Arg	Phe	Pro	Pro	Gln	965	970	975
Gln	Ala	Thr	Pro	Pro	Leu	Ile	Met	Glu	Glu	Arg	Pro	Asn	Leu	Tyr	Ser	980	985	990
Gln	Pro	Tyr	Ser	Ser	Pro	Phe	Pro	Thr	Ala	Asn	Leu	Pro	Ser	Pro	Phe	995	1000	1005
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Asn	Ala	Gln	Met	Leu	Ala	Gln	Arg	Gln	Arg	Glu	Leu	Tyr	Ser	Gln	Gln	1105	1110	1115
His	Arg	Gln	Arg	Gln	Leu	Ile	Gln	Gln	Gln	Arg	Ala	Met	Leu	Met	Arg	1125	1130	1135
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<220>
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